

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/759,256

Source: \_\_\_\_\_

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## RAW SEQUENCE LISTING

DATE: 03/03/2005

PATENT APPLICATION: US/10/759,256

TIME: 12:51:31

Input Set : N:\Crf3\RULE60\10759256.raw.txt

Output Set: N:\CRF4\03022005\J759256.raw

1 <110> APPLICANT: Conseiller, Emmanuel  
 2 Debussche, Laurent  
 3 Gallagher, William  
 4 <120> TITLE OF INVENTION: Polypeptide (MBP1) Capable Of Interacting With Oncogenic  
 Mutants Of The  
 5 P53 Protein  
 6 <130> FILE REFERENCE: ST98033  
 7 <140> CURRENT APPLICATION NUMBER: US/10/759,256  
 8 <141> CURRENT FILING DATE: 2004-01-20  
 9 <150> PRIOR APPLICATION NUMBER: US/09/829,936  
 10 <151> PRIOR FILING DATE: 2001-04-11  
 11 <150> PRIOR APPLICATION NUMBER: FR9812754  
 12 <151> PRIOR FILING DATE: 1998-10-12  
 13 <160> NUMBER OF SEQ ID NOS: 33  
 14 <170> SOFTWARE: PatentIn version 3.1  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 23  
 18 <212> TYPE: DNA  
 19 <213> ORGANISM: Artificial Sequence  
 20 <220> FEATURE:  
 21 <223> OTHER INFORMATION: Oligonucleotide 5'-1(p53)  
 22 <400> SEQUENCE: 1  
 23 agatctgtat ggaggagccg cag 23  
 25 <210> SEQ ID NO: 2  
 26 <211> LENGTH: 29  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Artificial Sequence  
 29 <220> FEATURE:  
 30 <223> OTHER INFORMATION: Oligonucleotide 3' -393 (p53)  
 31 <400> SEQUENCE: 2  
 32 agatctcatc agtctgagtc aggcccttc 29  
 34 <210> SEQ ID NO: 3  
 35 <211> LENGTH: 15  
 36 <212> TYPE: DNA  
 37 <213> ORGANISM: Artificial Sequence  
 38 <220> FEATURE:  
 39 <223> OTHER INFORMATION: Oligonucleotide H175 3'  
 40 <400> SEQUENCE: 3  
 41 ggggcagtgc ctcac 15  
 43 <210> SEQ ID NO: 4  
 44 <211> LENGTH: 15  
 45 <212> TYPE: DNA  
 46 <213> ORGANISM: Artificial Sequence  
 47 <220> FEATURE:

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48 <223> OTHER INFORMATION: Oligonucleotide W248 3'
49 <400> SEQUENCE: 4
50      gggcctccag ttcac                                     15
52 <210> SEQ ID NO: 5
53 <211> LENGTH: 15
54 <212> TYPE: DNA
55 <213> ORGANISM: Artificial Sequence
56 <220> FEATURE:
57 <223> OTHER INFORMATION: Oligonucleotide H273 3'
58 <400> SEQUENCE: 5
59      acaaacatgc acctc                                     15
61 <210> SEQ ID NO: 6
62 <211> LENGTH: 15
63 <212> TYPE: DNA
64 <213> ORGANISM: Artificial Sequence
65 <220> FEATURE:
66 <223> OTHER INFORMATION: Oligonucleotide G281 3'
67 <400> SEQUENCE: 6
68      gcgcgcgcct ctccc                                     15
70 <210> SEQ ID NO: 7
71 <211> LENGTH: 23
72 <212> TYPE: DNA
73 <213> ORGANISM: Artificial Sequence
74 <220> FEATURE:
75 <223> OTHER INFORMATION: Oligonucleotide 5'-73
76 <400> SEQUENCE: 7
77      agatctgtgt ggccccctgca cca                         23
79 <210> SEQ ID NO: 8
80 <211> LENGTH: 1021
81 <212> TYPE: DNA
82 <213> ORGANISM: Artificial Sequence
83 <220> FEATURE:
84 <223> OTHER INFORMATION: Murine MBP1 C-term fragment
85 <220> FEATURE:
86 <221> NAME/KEY: CDS
87 <222> LOCATION: (1)..(885)
88 <400> SEQUENCE: 8
89      tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtg gac      48
90      Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
91      1          5          10          15
92      ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac ctg      96
93      Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
94      20          25          30
95      ccg ggc tcc ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga cct      144
96      Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
97      35          40          45
98      aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc cca      192
99      Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
100     50          55          60

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101	tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgt	240
102	Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys	
103	65 70 75 80	
104	aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat atc	288
105	Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile	
106	85 90 95	
107	gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc aac	336
108	Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn	
109	100 105 110	
110	gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg ctg	384
111	Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu	
112	115 120 125	
113	gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca cac	432
114	Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His	
115	130 135 140	
116	caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac cgc	480
117	Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg	
118	145 150 155 160	
119	tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca gac	528
120	Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp	
121	165 170 175	
122	aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag cct	576
123	Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro	
124	180 185 190	
125	tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt gtg	624
126	Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val	
127	195 200 205	
128	cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt gcc	672
129	Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala	
130	210 215 220	
131	tac aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc tac	720
132	Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr	
133	225 230 235 240	
134	att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg cca	768
135	Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro	
136	245 250 255	
137	gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc atg	816
138	Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met	
139	260 265 270	
140	aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg gtc	864
141	Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val	
142	275 280 285	
143	ttt gtg gga gcc tat acc ttc tgaagaccct caggggaagg ccattgtggg	915
144	Phe Val Gly Ala Tyr Thr Phe	
145	290 295	
146	gcccccttccc cctcccatag cttaagcagc cccggggggcc tagggatgac cgttctgctt	975
147	aaaggaacta tgatgtgaag gacaataaag ggagaaagaa ggaaaa	1021
149	<210> SEQ ID NO: 9	
150	<211> LENGTH: 295	

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151 <212> TYPE: PRT
152 <213> ORGANISM: Artificial Sequence
153 <220> FEATURE:
154 <223> OTHER INFORMATION: Murine MBP1 C-term fragment
155 <400> SEQUENCE: 9
156   Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
157   1           5           10           15
158   Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
159           20           25           30
160   Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
161           35           40           45
162   Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
163           50           55           60
164   Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
165           65           70           75           80
166   Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
167           85           90           95
168   Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
169           100          105          110
170   Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
171           115          120          125
172   Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His
173           130          135          140
174   Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
175           145          150          155          160
176   Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp
177           165          170          175
178   Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro
179           180          185          190
180   Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val
181           195          200          205
182   Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
183           210          215          220
184   Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr
185           225          230          235          240
186   Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
187           245          250          255
188   Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
189           260          265          270
190   Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
191           275          280          285
192   Phe Val Gly Ala Tyr Thr Phe
193           290          295
195 <210> SEQ ID NO: 10
196 <211> LENGTH: 39
197 <212> TYPE: DNA
198 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Oligonucleotide c-myc 5'

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201 <400> SEQUENCE: 10
202     gatccatgga gcagaagctg atctccgagg aggacctga                      39
204 <210> SEQ ID NO: 11
205 <211> LENGTH: 39
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: Oligonucleotide c-myc 3'
210 <400> SEQUENCE: 11
211     gatctcaggt cctcctcgga gatcagcttc tgctccatg                      39
213 <210> SEQ ID NO: 12
214 <211> LENGTH: 45
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: 5' MCS oligonucleotide
219 <400> SEQUENCE: 12
220     gatctcggtc gacctgcatg caattcccgg gtgcggccgc gagct              45
222 <210> SEQ ID NO: 13
223 <211> LENGTH: 37
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: 3' MCS oligonucleotide
228 <400> SEQUENCE: 13
229     cgcggccgca cccgggaatt gcatgcaggt cgaccga                      37
231 <210> SEQ ID NO: 14
232 <211> LENGTH: 22
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Oligonucleotide 3' mMBP1
237 <400> SEQUENCE: 14
238     cggtactggc agaggtaact gg                                          22
240 <210> SEQ ID NO: 15
241 <211> LENGTH: 1513
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
245 <223> OTHER INFORMATION: MBP1 murine (complete sequence)
246 <220> FEATURE:
247 <221> NAME/KEY: CDS
248 <222> LOCATION: (49)..(1377)
249 <400> SEQUENCE: 15
250     gctgtggcag aaaccctga cttctgcccc ccacctccca gcctcagg atg ctc cct    57
251                                     Met Leu Pro
252                                     1
253     ttt gcc tcc tgc ctc ccc ggg tct ttg ctg ctc tgg gcg ttt ctg ctg    105
254     Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala Phe Leu Leu

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

**VERIFICATION SUMMARY**

**PATENT APPLICATION: US/10/759,256**

**DATE: 03/03/2005**

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**Input Set : N:\Crf3\RULE60\10759256.raw.txt**

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